

Report

	assembly
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	9623071
Total length (>= 5000 bp)	9618764
Total length (>= 10000 bp)	9609490
Total length (>= 25000 bp)	9582435
Total length (>= 50000 bp)	9546358
# contigs	8
Largest contig	4724719
Total length	9623071
Reference length	4875441
GC (%)	51.32
Reference GC (%)	50.49
N50	4711651
NG50	4724719
N75	4711651
NG75	4724719
L50	2
LG50	1
L75	2
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 2 part
Unaligned length	4615552
Genome fraction (%)	100.000
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.25
# indels per 100 kbp	36.47
Largest alignment	4724719
Total aligned length	5007570
NA50	109988
NGA50	4724719
NGA75	4724719
LA50	2
LGA50	1
LGA75	1

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

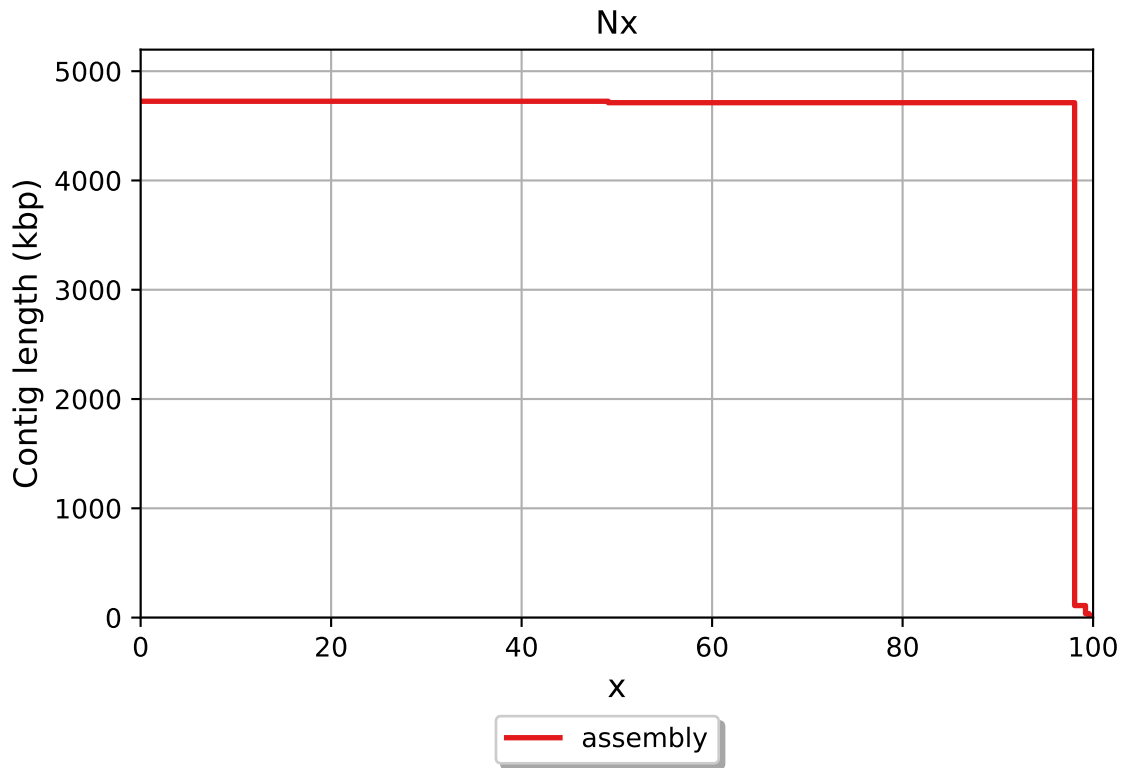
	assembly
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	3035
# indels	1778
# indels (<= 5 bp)	1773
# indels (> 5 bp)	5
Indels length	2038

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

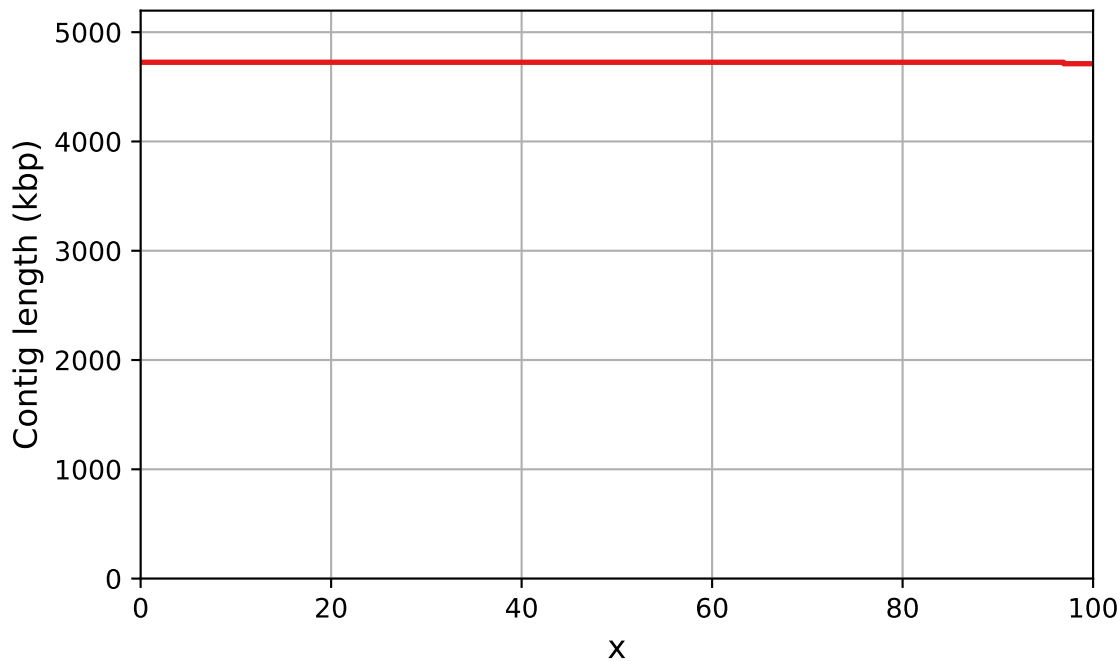
Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	4615552
# N's	0

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

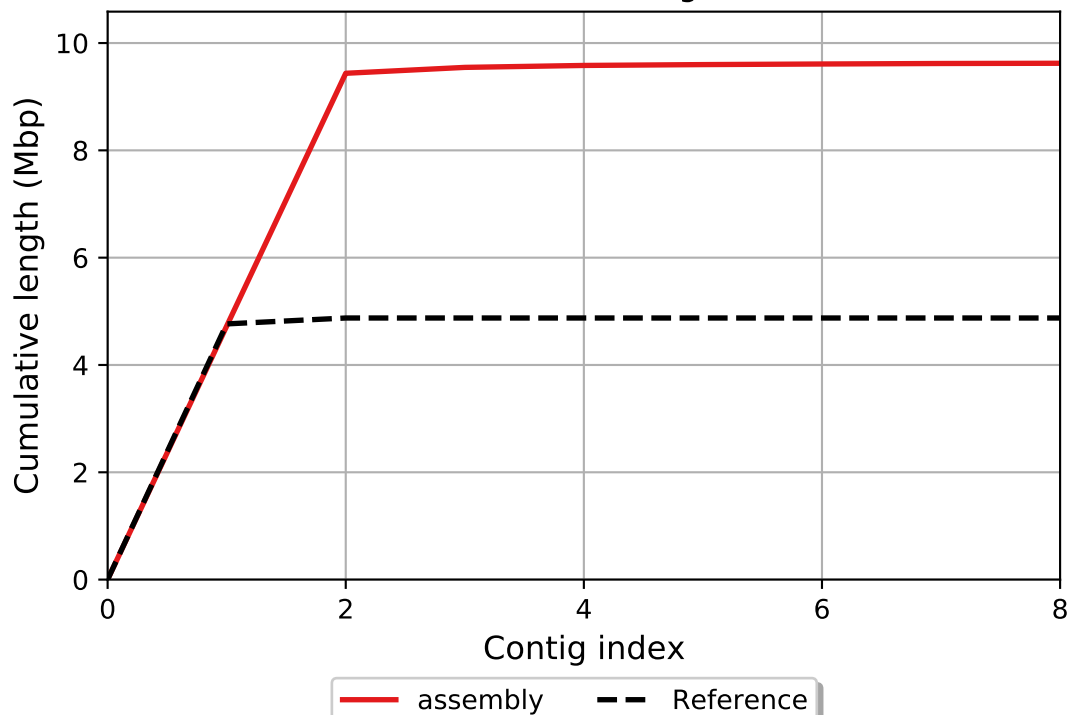


NGx

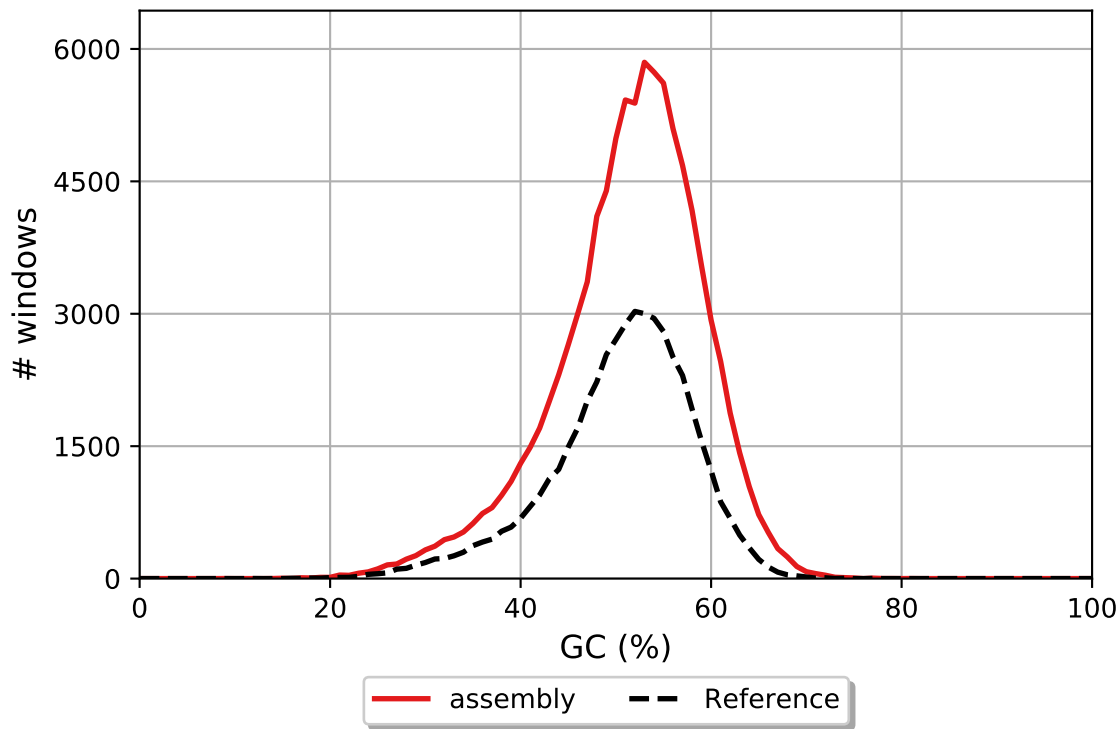


— assembly

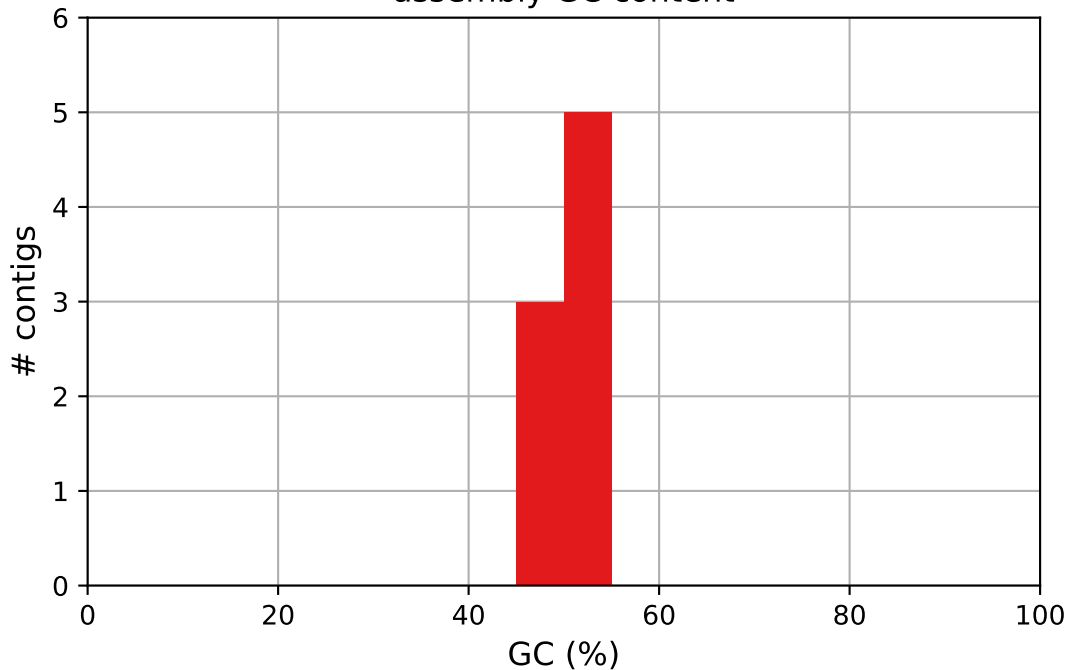
Cumulative length



GC content

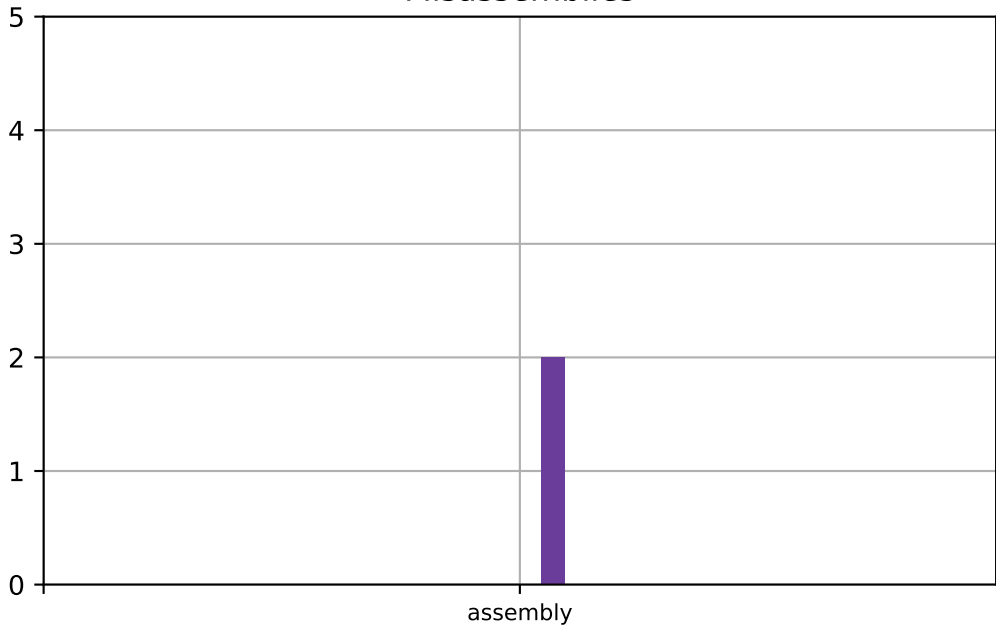


assembly GC content



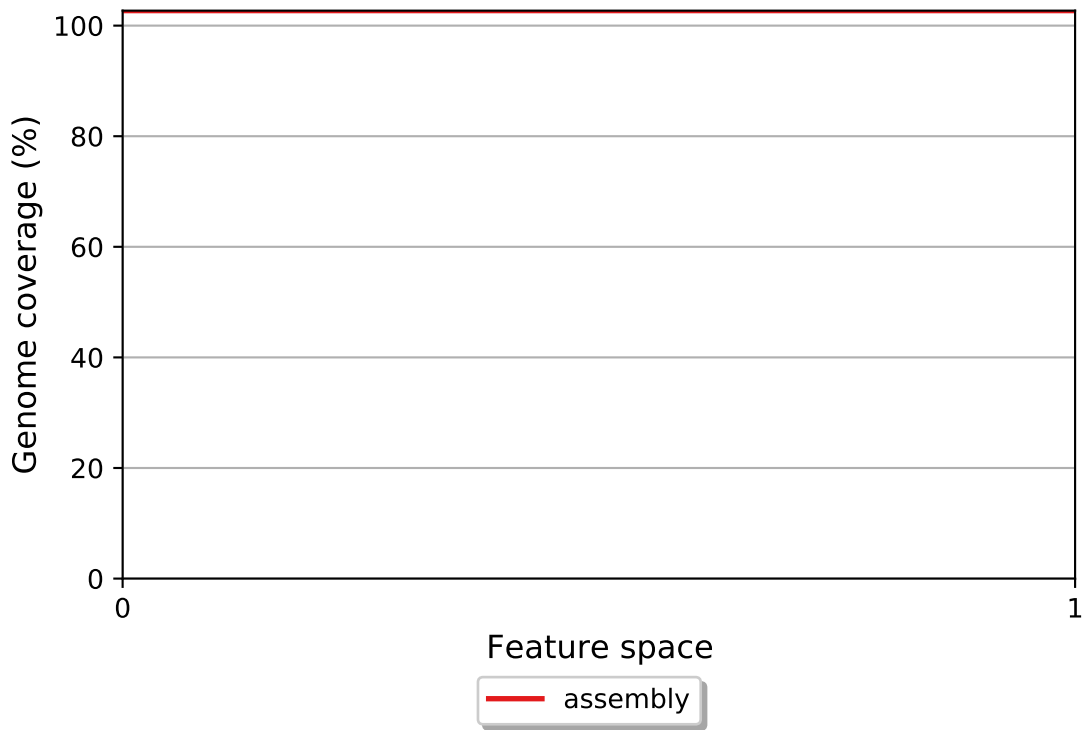
assembly

Misassemblies

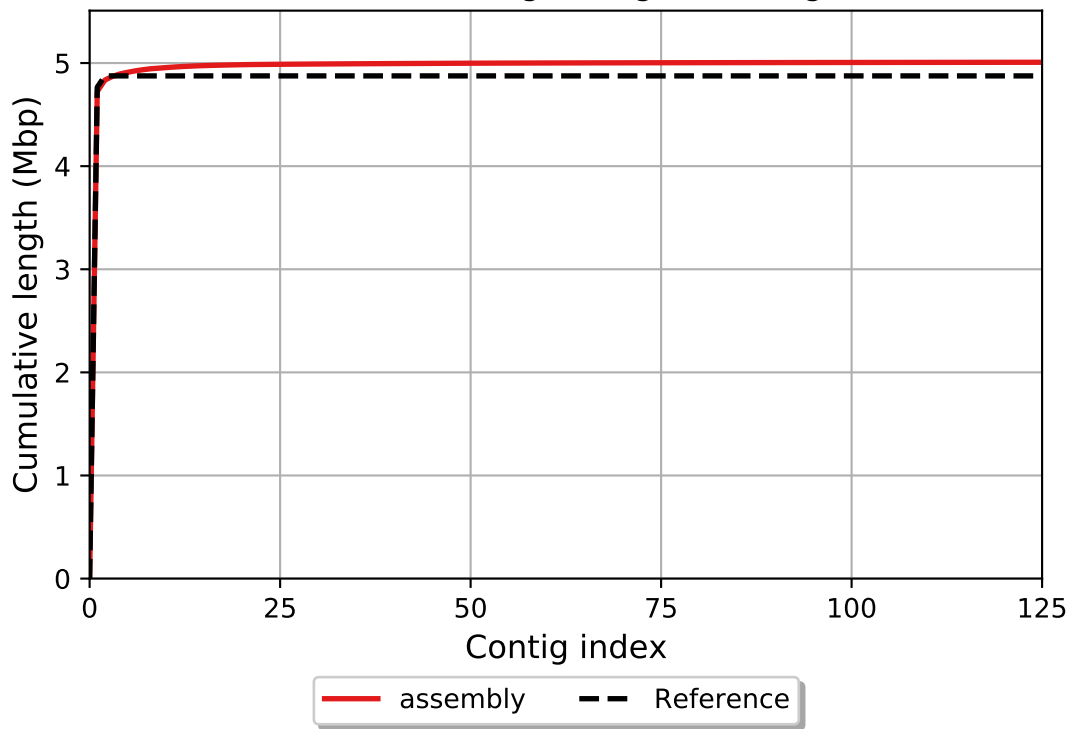


interspecies translocations

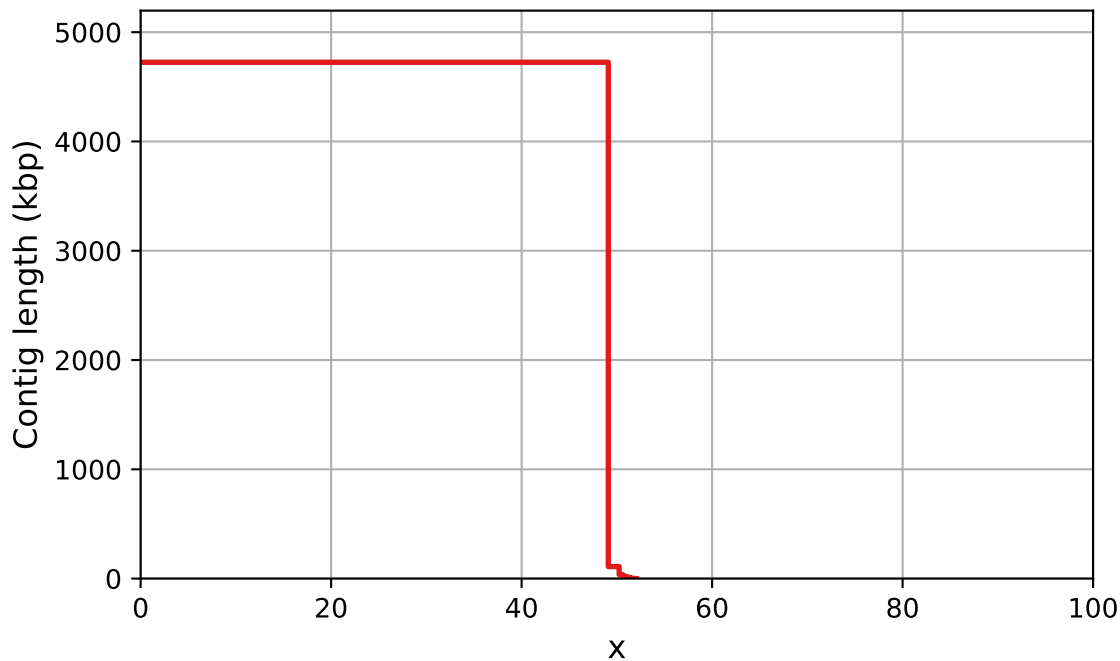
FRCurve (misassemblies)



Cumulative length (aligned contigs)

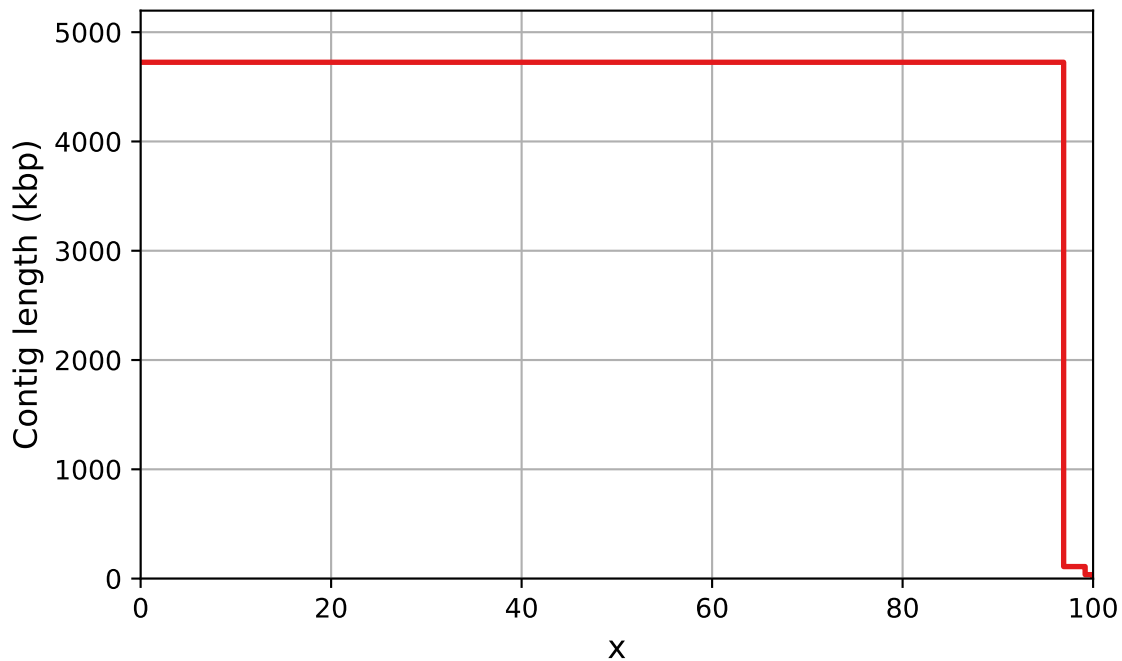


NAx



— assembly

NGAx



— assembly